

#14



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1600

RAW SEQUENCE LISTING

DATE: 03/14/2003

PATENT APPLICATION: US/09/744,125A

TIME: 12:04:51

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Output Set : N:\CRF4\03142003\I744125A.raw

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3 <110> APPLICANT: Marcireau, Christophe
4      Multon, Marie-Christine
5      Polard-Houset, Valerie
7 <120> TITLE OF INVENTION: MEKK1-INTERACTING FHA PROTEIN
9 <130> FILE REFERENCE: A3233
11 <140> CURRENT APPLICATION NUMBER: 09/744,125A
12 <141> CURRENT FILING DATE: 2001-01-19
14 <150> PRIOR APPLICATION NUMBER: PCT/EP99/05142
15 <151> PRIOR FILING DATE: 1999-07-21
17 <150> PRIOR APPLICATION NUMBER: 60/093,590
18 <151> PRIOR FILING DATE: 1998-07-21
20 <160> NUMBER OF SEQ ID NOS: 16
22 <170> SOFTWARE: PatentIn version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1553
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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34 ccctggactc accaagcgtg tgaagaagag taacacagcca cttcaggtga ccaaggatct      180
36 gggccgctgg aagcctgcaa atgacctcct gctcataaat gctgtgttgc agaccaacga      240
38 cctgacctcc gtccacctgg gcgtgaaatt cagctgccgc ttcacccttc gggaggtcca      300
40 ggagcgttgg tacgccctgc tctacgatcc tgtcatctcc aagttggcct gtcaggccat      360
42 gaggcagctg caccagagg ctattgcagc catccagagc aaggccctgt ttagcaaggc      420
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46 ggacctgctg cacagacacc ctgatgcctt ctacctggcc cgtaccgcga aggccttcca      540
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50 gcccaaaggg gaccaagtgc tgaacttctc tgatgcagag gacctgattg atgacagtaa      660
52 gctcaaggac atgcgagatg aggtcctgga acatgagctg atgggtggctg accggcgcca      720
54 gaagcgagag attcggcagc tggaacagga actgcataag tggcaggtgc tagtggacag      780
56 catcacaggc atgagctctc cggacttcga caaccagaca ctggcagtg ctcggggccg      840
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60 ccagattgat gtggacctgt ctctggaggg tccggcctgg aagatatccc ggaaacaagg      960
62 tgtcatcaag ctgaagaaca acggtgattt cttcattgcc aatgagggtc gacggcccat      1020
64 ctacatcgat ggacggccgg tgctctgtgg ctccaaatgg cgctcagca acaactctgt      1080
66 ggtggagatc gccagcctgc gattcgtctt ccttatcaac caggacctca ttgccctcat      1140
68 cagggtgag gctgccaaag tcacaccaca gtgaggaatg gtggcaggac tcgtgggccc      1200
70 tctccggcct gtttccccct ccactccagc ccccttgagc tgggaactca ggctcctgga      1260
72 aaaacctggg cagtgaggag ctcagctgcg ggccattgat ttgagccttt gagggaggat      1320
74 agggctggcc tttgtgaagc cagcagaggc tgagaacctc aggcctccct agatccagag      1380
76 cccctcccca tcttctcttc tctaaaaaca accctacccc ccattctacc cccattgcc      1440
78 accttcactc ctgtgtctcc agctgattag cctcagactc ttcttttatt gtttttcttt      1500

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83 <210> SEQ ID NO: 2

84 <211> LENGTH: 390

85 <212> TYPE: PRT

86 <213> ORGANISM: Homo sapiens

88 <400> SEQUENCE: 2

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91 1 5 10 15

93 Pro Ser Ser Ser Glu Lys Lys Lys Val Ser Lys Ala Pro Ser Thr Pro

94 20 25 30

96 Val Pro Pro Ser Pro Ala Pro Ala Pro Gly Leu Thr Lys Arg Val Lys

97 35 40 45

99 Lys Ser Lys Gln Pro Leu Gln Val Thr Lys Asp Leu Gly Arg Trp Lys

100 50 55 60

102 Pro Ala Asn Asp Leu Leu Leu Ile Asn Ala Val Leu Gln Thr Asn Asp

103 65 70 75 80

105 Leu Thr Ser Val His Leu Gly Val Lys Phe Ser Cys Arg Phe Thr Leu

106 85 90 95

108 Arg Glu Val Gln Glu Arg Trp Tyr Ala Leu Leu Tyr Asp Pro Val Ile

109 100 105 110

111 Ser Lys Leu Ala Cys Gln Ala Met Arg Gln Leu His Pro Glu Ala Ile

112 115 120 125

114 Ala Ala Ile Gln Ser Lys Ala Leu Phe Ser Lys Ala Glu Glu Gln Leu

115 130 135 140

117 Leu Ser Lys Val Gly Ser Thr Ser Gln Pro Thr Leu Glu Thr Phe Gln

118 145 150 155 160

120 Asp Leu Leu His Arg His Pro Asp Ala Phe Tyr Leu Ala Arg Thr Ala

121 165 170 175

123 Lys Ala Leu Gln Ala His Trp Gln Leu Met Lys Gln Tyr Tyr Leu Leu

124 180 185 190

126 Glu Asp Gln Thr Val Gln Pro Leu Pro Lys Gly Asp Gln Val Leu Asn

127 195 200 205

129 Phe Ser Asp Ala Glu Asp Leu Ile Asp Asp Ser Lys Leu Lys Asp Met

130 210 215 220

132 Arg Asp Glu Val Leu Glu His Glu Leu Met Val Ala Asp Arg Arg Gln

133 225 230 235 240

135 Lys Arg Glu Ile Arg Gln Leu Glu Gln Glu Leu His Lys Trp Gln Val

136 245 250 255

138 Leu Val Asp Ser Ile Thr Gly Met Ser Ser Pro Asp Phe Asp Asn Gln

139 260 265 270

141 Thr Leu Ala Val Leu Arg Gly Arg Met Val Arg Tyr Leu Met Arg Ser

142 275 280 285

144 Arg Glu Ile Thr Leu Gly Arg Ala Thr Lys Asp Asn Gln Ile Asp Val

145 290 295 300

147 Asp Leu Ser Leu Glu Gly Pro Ala Trp Lys Ile Ser Arg Lys Gln Gly

148 305 310 315 320

150 Val Ile Lys Leu Lys Asn Asn Gly Asp Phe Phe Ile Ala Asn Glu Gly

151 325 330 335

153 Arg Arg Pro Ile Tyr Ile Asp Gly Arg Pro Val Leu Cys Gly Ser Lys

100% 77-462 of Ren protein
AF015308

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154          340          345          350
156 Trp Arg Leu Ser Asn Asn Ser Val Val Glu Ile Ala Ser Leu Arg Phe
157          355          360          365
159 Val Phe Leu Ile Asn Gln Asp Leu Ile Ala Leu Ile Arg Ala Glu Ala
160          370          375          380
162 Ala Lys Ile Thr Pro Gln
163 385          390
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 669
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Sequence of the insert of the plasmid pCM524
173 <400> SEQUENCE: 3
174 gaattcggca cgagcattaa acttatacat gtatttttagg tttctgctat ggcagggtatt      60
176 ttttgtttca aagaacgaat ttctgttaaa taaagttata gtagctattg taacaaataa      120
178 atcctcaaat atgagtgggt taacatttat ataaagttaa aaacataggt taccaattag      180
180 ctgggagctc tcatccaagt ggtgattcag taatccaggc tcctttcatt ttgtggctcc      240
182 tctatattca acatataact actgaagtca ttgctgacag cagcatggga aatcccagta      300
184 ggaatttttt tatgggataa ccttgggaagt attgcccac acttcctcct aaattctatt      360
186 gttcagaaat cagacacaaa atctcactta agcaaggaag cctgaaaaat gtagtagaac      420
188 tgtgtgatta ggagaaagta atgggttttg tgagtacgta ttagtatctc tcacattggg      480
190 agaaatggct ttttatatgt ttttaagaaa caaattttgt tatctttctc tccattggct      540
192 ccattgcccc agcaaagtag tagaacaaaa ataatatatt ttaaaattta acattatata      600
194 ttaatgataa tgcttaaaca gttgtattta cctgtttcaa aaagaaaaaa aaaaaaaaaa      660
196 aaactcgag                                         669
199 <210> SEQ ID NO: 4
200 <211> LENGTH: 128
201 <212> TYPE: PRT
202 <213> ORGANISM: Artificial
204 <220> FEATURE:
205 <223> OTHER INFORMATION: deduced amino acid sequence of the insert of the plasmid
pCM524
208 <400> SEQUENCE: 4
210 Asn Ser Ala Arg Glu Arg Arg Gln Arg Glu Glu Arg Arg Gln Ser Asn
211 1          5          10          15
213 Leu Gln Glu Val Leu Glu Arg Glu Arg Arg Glu Leu Glu Lys Leu Tyr
214          20          25          30
216 Gln Glu Arg Lys Met Ile Glu Glu Ser Leu Lys Ile Lys Ile Lys Lys
217          35          40          45
219 Glu Leu Glu Met Glu Asn Glu Leu Glu Met Ser Asn Gln Glu Ile Lys
220          50          55          60
222 Asp Lys Ser Ala His Ser Glu Asn Pro Leu Glu Lys Tyr Met Lys Ile
223 65          70          75          80
225 Ile Gln Gln Glu Gln Asp Gln Glu Ser Ala Asp Lys Ser Ser Lys Lys
226          85          90          95
228 Met Val Gln Glu Gly Ser Leu Val Asp Thr Leu Gln Ser Ser Asp Lys
229          100         105         110
231 Val Glu Ser Leu Thr Gly Phe Ser His Glu Glu Leu Asp Asp Ser Trp
232          115         120         125

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Input Set : A:\A3233seq1t.txt

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234 <210> SEQ ID NO: 5
235 <211> LENGTH: 669
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Insert of plasmid pCM482
242 <400> SEQUENCE: 5
243 gaattcggca cgagcattaa acttatacat gtattttagg tttctgctat ggcagggtatt      60
245 ttttgtttca aagaacgaat ttctgttaaa taaagttata gtagctattg taacaaataa      120
247 atcctcaa atgagtgggt taacatttat ataaagtga aaacatagggt taccaattag      180
249 ctgggagctc tcattccaagt ggtgattcag taatccaggc tcctttcatt ttgtggctcc      240
251 tctatattca acataaact actgaagtca ttgctgacag cagcatggga aatcccagta      300
253 ggaatttttt tatgggataa ccttgggaagt attgcccac acttcctcct aaattctatt      360
255 gttcagaaat cagacacaaa atctcactta agcaaggaag cctgaaaaat gtagtagaac      420
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259 agaaatggct ttttatatgt ttttaagaaa caaattttgt tatctttctc tccattggct      540
261 ccattgcccc agcaaagtag tagaacaaaa ataatatatt ttaaaattta acattatata      600
263 ttaatgataa tgcttaaaca gttgtattta cctgtttcaa aaagaaaaaa aaaaaaaaaa      660
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268 <210> SEQ ID NO: 6
269 <211> LENGTH: 50
270 <212> TYPE: PRT
271 <213> ORGANISM: Artificial
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Deduced amino acid sequence of insert of plasmid pCM482
276 <400> SEQUENCE: 6
278 Asn Ser Ala Arg Ala Leu Asn Leu Tyr Met Tyr Phe Arg Phe Leu Leu
279 1      5      10      15
281 Trp Gln Val Phe Phe Val Ser Lys Asn Glu Phe Leu Leu Asn Lys Val
282      20      25      30
284 Ile Val Ala Ile Val Thr Asn Lys Ser Ser Asn Met Ser Gly Leu Thr
285      35      40      45
287 Phe Ile
288      50
290 <210> SEQ ID NO: 7
291 <211> LENGTH: 1914
292 <212> TYPE: DNA
293 <213> ORGANISM: Murinae gen. sp.
295 <400> SEQUENCE: 7
296 cgcgagaaaa ttgttggtatc tggcagtcta ggaatgaatc tcctctcagc ctttaagctc      60
298 acctggtcag aatccttgga tgagcctgtg ggaccgttcc tcctagcccg gtggtttgga      120
300 accagtggct ttgggactgt aagaggatgg acaaagattc tcaggggctg ctagattcat      180
302 cctgatggc atcaggcact gccagccgct cagaggatga ggagtcactg gcagggcaga      240
304 agcgagcctc ctcccaggcc ttgggcacca tccctaaacg gagaagctcc tccaggttca      300
306 tcaagaggaa gaagttcgat gatgactgg tgagagcag cctggcaaaa tcttctaccc      360
308 gggcaaaagg ggccagtgg gtggaaccag ggcgtgttc ggggagtga cctcctcca      420
310 gtgagaagaa gaaggtatcc aaagcccca gcaactcgtt gccaccagc ccagccccag      480
312 cccctggact caccaagcgt gtgaagaaga gtaaacagcc acttcagggt accaaggatc      540
314 tgggccgctg gaagcctgca gatgacctcc tgctcataaa tgctgtgttg cagaccaacg      600

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316 acctgacctc cgtccacctg ggcgtgaaat tcagctgccg cttcacccctt cgggaggtcc 660
318 aggagcggtt gtagcgccctg ctctacgatc ctgtcatctc caagttggcc tgtcaggcca 720
320 tgaggcagct gcacccagag gctattgcag ccatccagag caaggccctg tttagcaagg 780
322 ctgaggagca gctgctgagc aaagtgggat cgaccagcca gccacacctg gagaccttcc 840
324 aggacctgct gcacagacac cctgatgcct tctacctggc ccgtaccgag aaggccctgc 900
326 aggcccactg gcagctcatg aagcagtatt acctgctgga ggaccagaca gtgcagccgc 960
328 tgcccaaagg ggaccaagtg ctgaacttct ctgatgcaga ggacctgatt gatgacagta 1020
330 agctcaagga catgcgagat gaggtcctgg aacatgagct gatggtggct gaccggcgcc 1080
332 agaagcgaga gattcggcag ctggaacagg aactgcataa gtggcaggtg ctagtggaca 1140
334 gcatcacagg catgagctct cgggacttcg acaaccagac actggcagtg ctgcggggcc 1200
336 gcatggtgag gtacctgatg cgctcgcgtg agatcacctt gggcagagca accaaggata 1260
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342 tctacatcga tggacggccg gtgctctgtg gctocaaatg gcgcctcagc aacaactctg 1440
344 tgggtggagat cgccagcctg cgattcgtct tccttatcaa ccaggacctc attgccctca 1500
346 tcagggtgta ggctgccaaag atcacaccac agtgaggaat ggtggcagga ctctgtggcc 1560
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354 gccctcccc atcttctct ctctaaaaac aacctaccc ccattctac ccccatctgc 1800
356 caccttcaact cctgtgtctc cagctgatta gcctcagact cttcttttat tgttttctt 1860
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361 <210> SEQ ID NO: 8

362 <211> LENGTH: 462

363 <212> TYPE: PRT

364 <213> ORGANISM: Murinae gen. sp.

366 <400> SEQUENCE: 8

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371 Gly Thr Ala Ser Arg Ser Glu Asp Glu Glu Ser Leu Ala Gly Gln Lys
372 20 25 30
374 Arg Ala Ser Ser Gln Ala Leu Gly Thr Ile Pro Lys Arg Arg Ser Ser
375 35 40 45
377 Ser Arg Phe Ile Lys Arg Lys Lys Phe Asp Asp Glu Leu Val Glu Ser
378 50 55 60
380 Ser Leu Ala Lys Ser Ser Thr Arg Ala Lys Gly Ala Ser Gly Val Glu
381 65 70 75 80
383 Pro Gly Arg Cys Ser Gly Ser Glu Pro Ser Ser Ser Glu Lys Lys Lys
384 85 90 95
386 Val Ser Lys Ala Pro Ser Thr Pro Val Pro Pro Ser Pro Ala Pro Ala
387 100 105 110
389 Pro Gly Leu Thr Lys Arg Val Lys Ser Lys Gln Pro Leu Gln Val
390 115 120 125
392 Thr Lys Asp Leu Gly Arg Trp Lys Pro Ala Asp Asp Leu Leu Leu Ile
393 130 135 140
395 Asn Ala Val Leu Gln Thr Asn Asp Leu Thr Ser Val His Leu Gly Val
396 145 150 155 160
398 Lys Phe Ser Cys Arg Phe Thr Leu Arg Glu Val Gln Glu Arg Trp Tyr
399 165 170 175

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VERIFICATION SUMMARY

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